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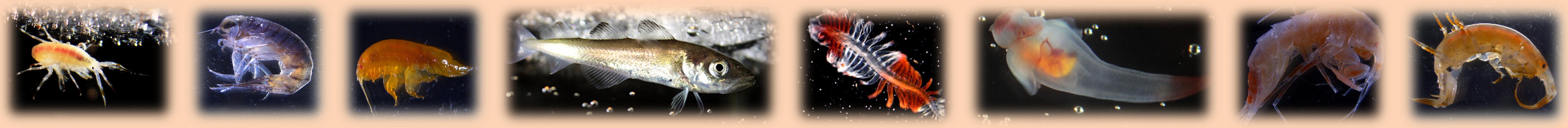
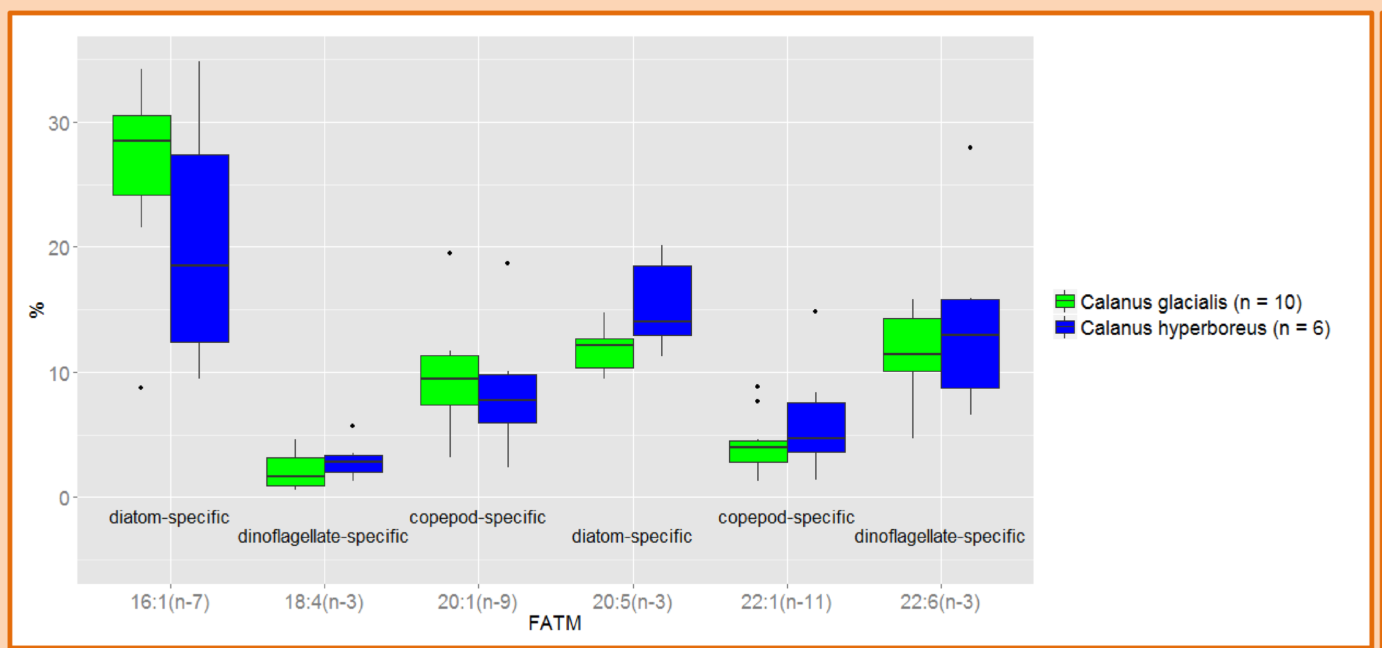
Tracing ice algae-produced carbon in a changing Arctic Ocean using biomarker analyses

The underside of sea ice in polar regions represents a natural habitat for heterotrophic organisms, e.g. copepods and amphipods. These organisms constitute the under-ice community, which plays a key role in transferring ice algae-produced carbon into pelagic and benthic food webs of polar ecosystems. Animals at higher trophic levels show an indirect dependency on microalgae-produced biomass. In order to improve our understanding of the potential ecological consequences of a changing sea ice environment, we aim to quantify the extent to which ice algae-produced carbon is channelled into the under-ice community, and from there to pelagic food webs.



1. Based on fatty acid patterns, copepods *Calanus glacialis* and *Calanus hyperboreus* were feeding on both, ice algae and pelagic phytoplankton.
Several amphipod species demonstrated high amounts of diatom-related fatty acids. (**Fig. 1, 2**).



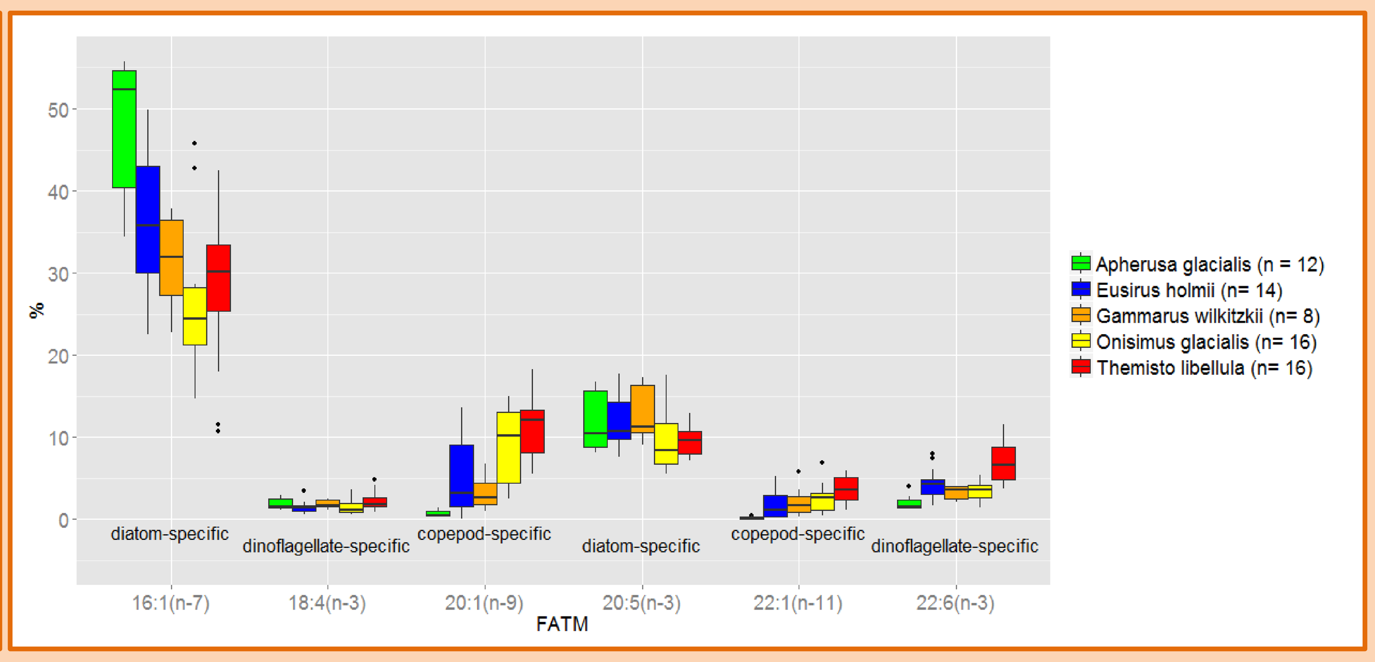
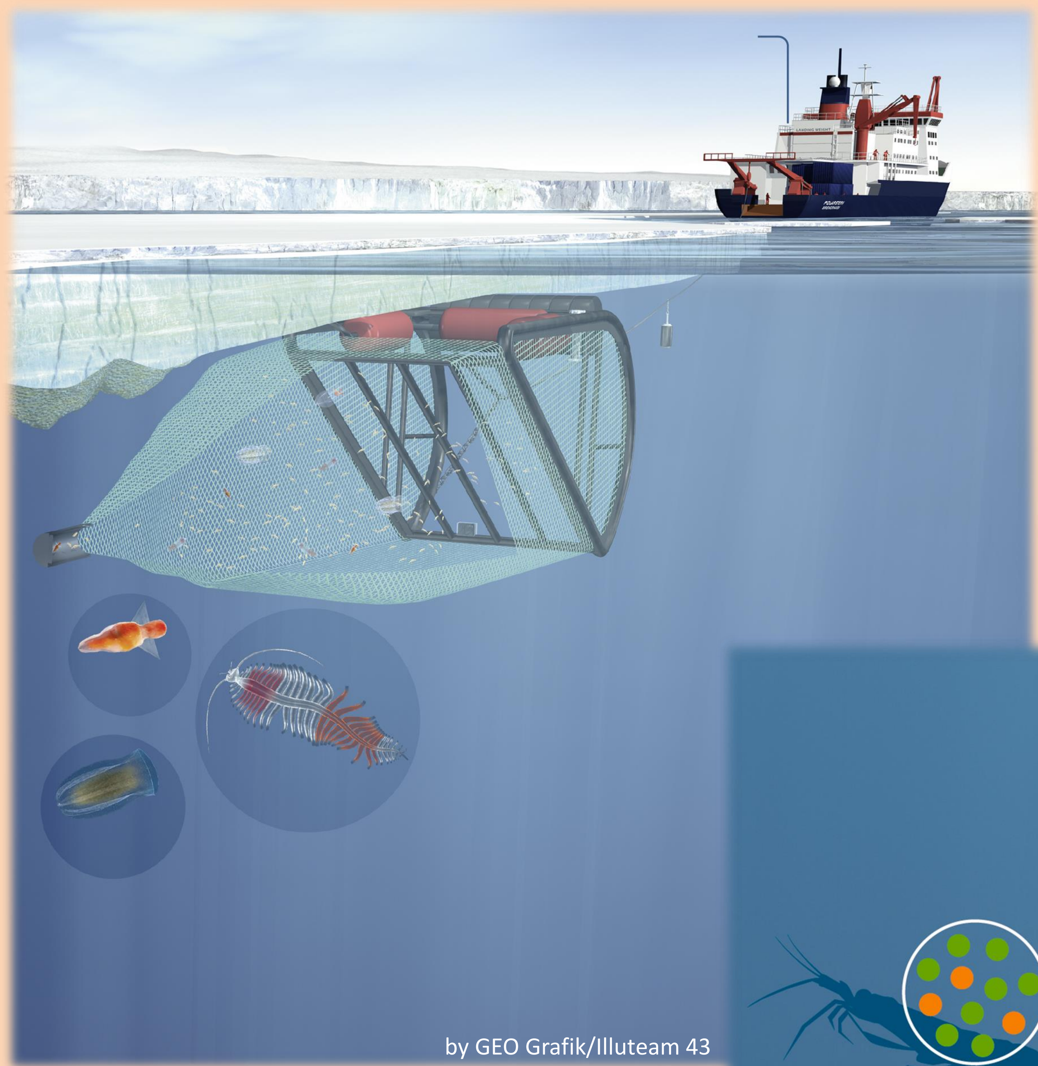


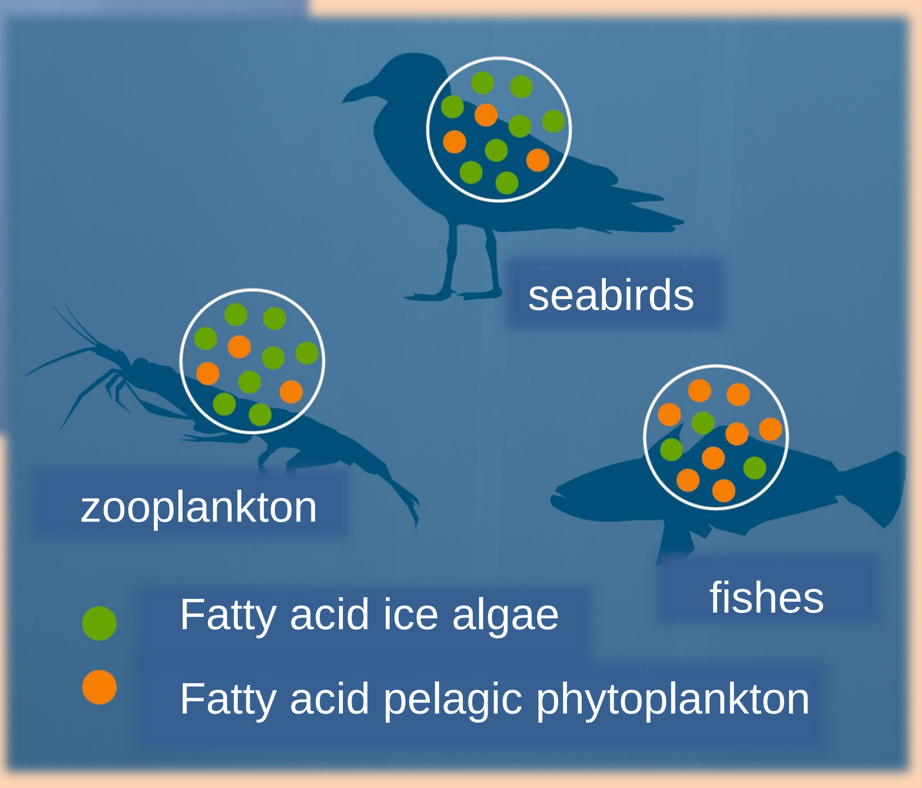
Fig. 1 (left). FATM (Fatty Acid Trophic Marker) proportions of copepods defined on the total fatty acid content (ordered by increasing chain length and number of unsaturation). Fatty acids were extracted[1,2] and separated by gas chromatography. Certain fatty acids are not biotransformed by consumers and therefore originally traceable along marine food chains.
Fig. 2 (right). FATM levels of abundant amphipod species.

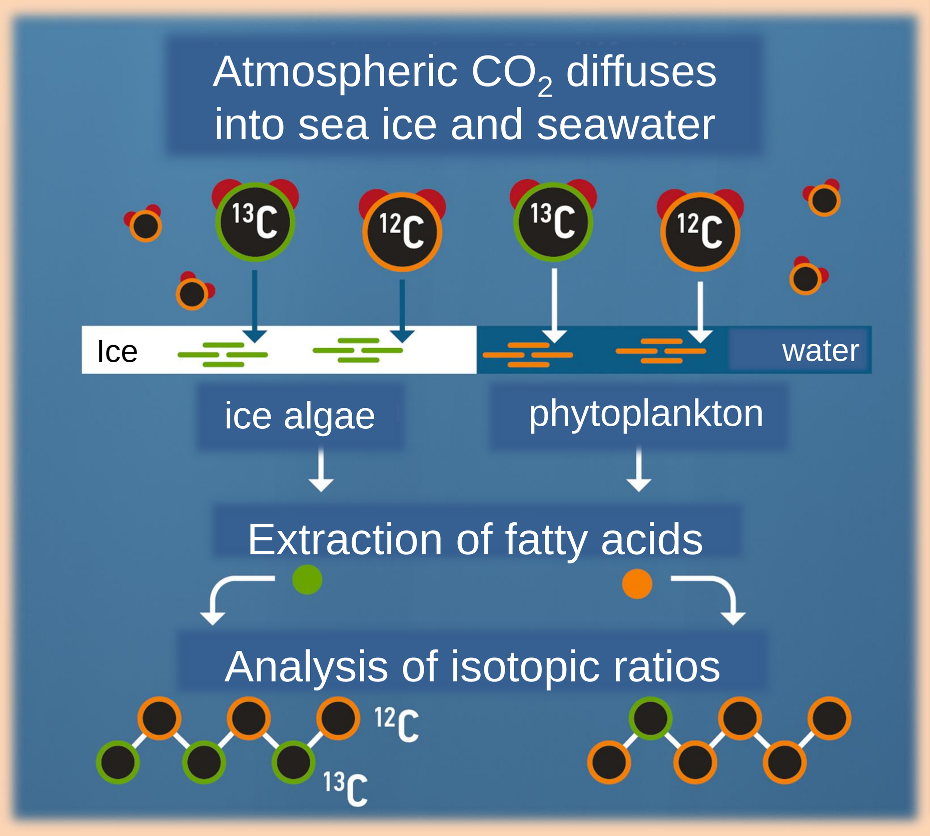
***BUT*: Taxonomic composition of ice algae and phytoplankton communities can be similar, e. g. diatoms can occur in both communities → for clarifying trophic relationships, stable isotope analysis can provide a valuable tool**



Sample collection was carried out during ARK XXVII-3 expedition of RV Polarstern (August-September 2012) within the Eastern Central Arctic Ocean north of 80°N. The under-ice habitat was sampled by the SUIT, the Surface and Under-Ice Trawl[3].

Methods.
Trophic interactions of abundant under-ice zooplankton were studied using **stable isotope analysis (SIA)** of natural abundance carbon and nitrogen[4], **lipid fingerprinting**, and **compound-specific SIA (CSIA)** of fatty acid trophic markers (FATM)[5].





2. Consumers with higher $\delta^{15}N$ ratios occupy higher trophic levels. Less negative $\delta^{13}C$ ratios indicate an ice algae-dominated diet (**Fig. 3**).

3. $\delta^{13}C$ ratios of FATM **20:5n-3** emphasize a strongly ice algae-related diet for some amphipods, and a mixed diet for copepods (**Fig. 4**).

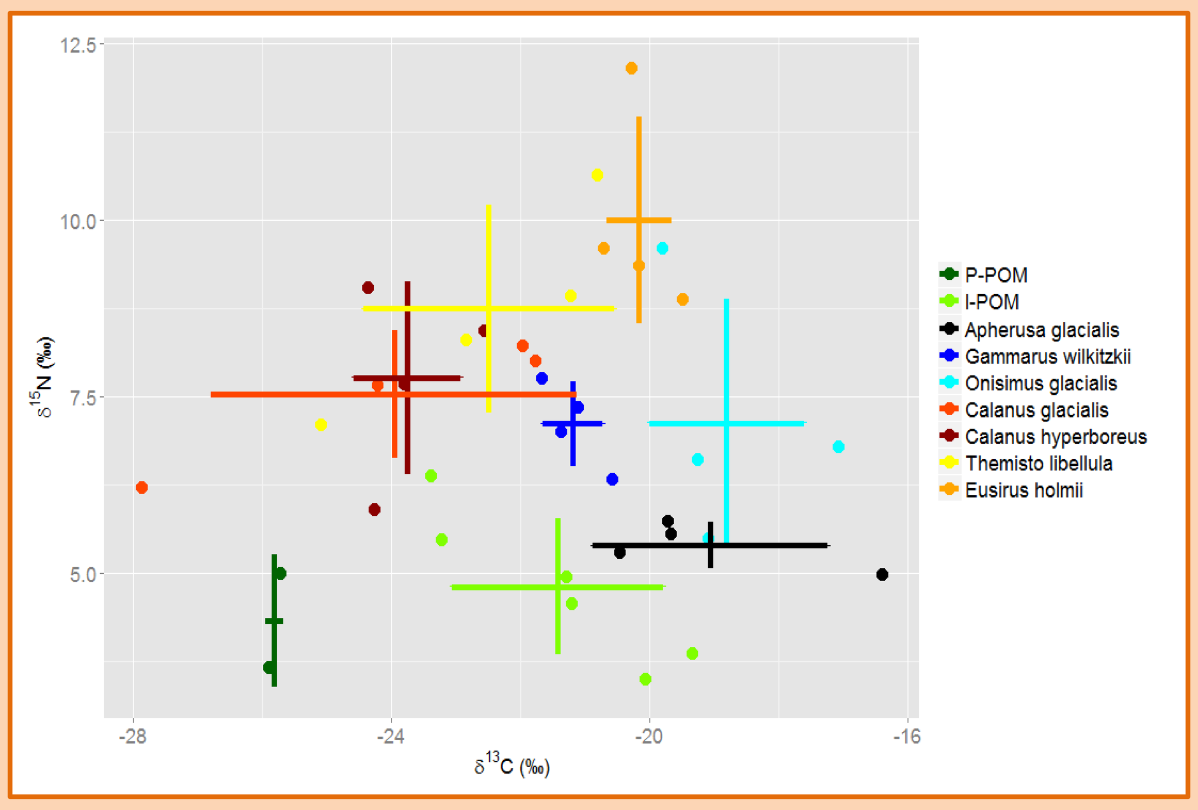
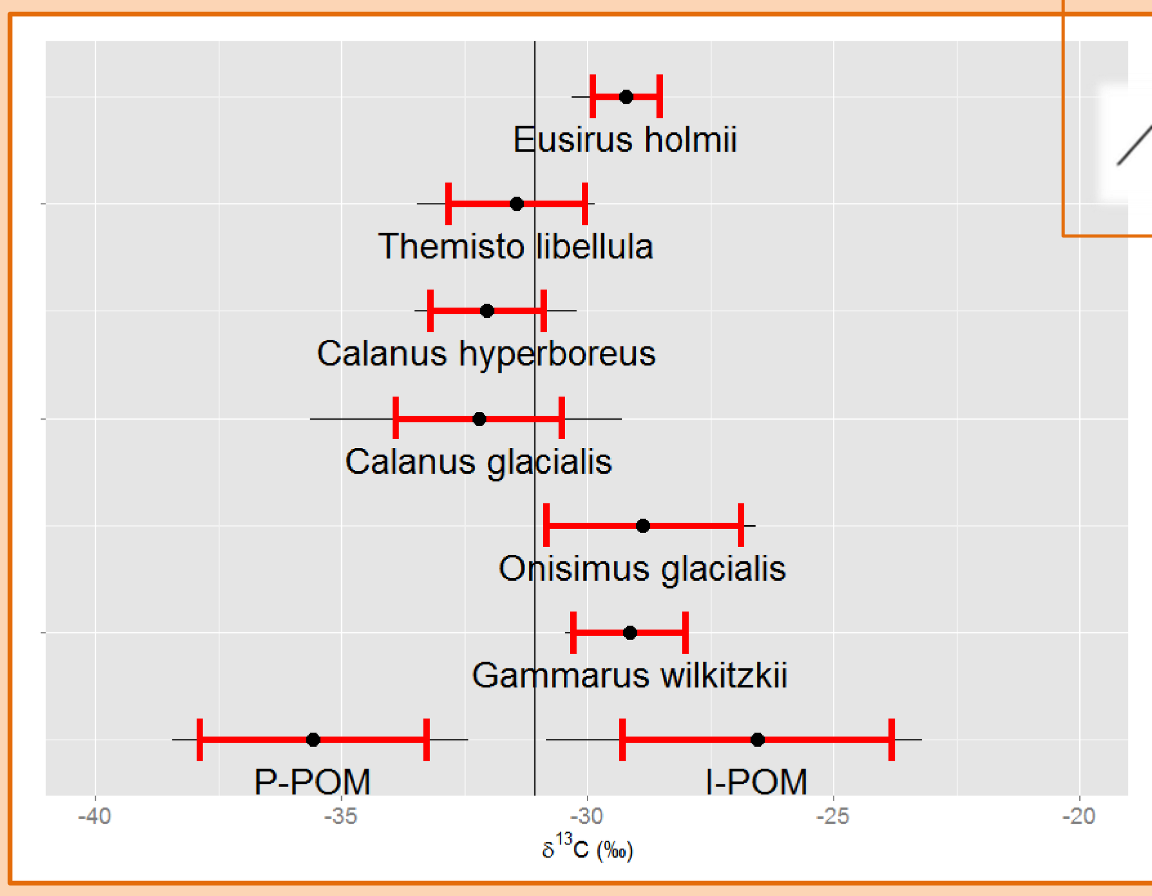


Fig. 3. Bulk stable isotope analysis of nitrogen and carbon compounds. Isotopic ratios are expressed as: $\delta X = [(R_{Sample}/R_{Standard})-1] \times 1000$, where X is $\delta^{13}C$ or $\delta^{15}N$ and R_{Sample} represents $^{13}C/^{12}C$ or $^{15}N/^{14}N$ relative to international standards. Pelagic phytoplankton is abbreviated as P-POM, ice algae as I-POM.



Omega-3 polyunsaturated fatty acid Eicoso-pentaenoic acid (EPA) **20:5n-3**[6]

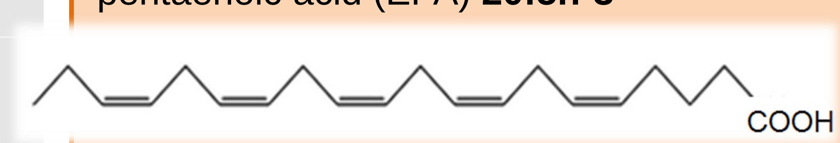


Fig. 4. Compound-specific stable isotope analysis of diatom-specific fatty acid **20:5n-3**. Pelagic phytoplankton is abbreviated as P-POM, ice algae as I-POM.

Iceflux project-
Ice-ecosystem carbon flux in polar oceans

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